Job Offer: **Computational Research Assistant**

Where
Computational Biology department at the Centre for Plant Genomics and Biotechnology (CBGP) in Madrid, Spain

About the Institute
The Centre for Plant Genomics and Biotechnology (CBGP) is a joint (UPM-INIA) research institute of excellence located at the Montegancedo International Campus in Pozuelo de Alarcón, Madrid. Research activities at the CBGP are focused on plant biology and associated microorganisms. CBGP has relevant educational and training roles for Bachelor, Master and PhD students, and technicians, and has contributed to impulse the scientific carrier and leadership of young scientists.

The center has a main building of 7,200 m2 with state of the art laboratories and scientific infrastructures, including metabolomics facilities, a high performance computing cluster, cell biology platforms and a P3-level containment lab.

Job Description
We are looking for a motivated person to join the Computational Program at CBGP (Madrid). The successful candidate will provide technical (*mostly programming*) support in the maintenance and further development of several bioinformatic resources, including the following tools and databases:

EggNOG Database[1]: a phylogenomic resource developed in collaboration with several international partners (http://eggnogdb.embl.de). Activities will include data updates for new releases, as well as front-end and API improvements.
Technologies used: Python, Javascript (angular), MongoDB.

ETE Toolkit[2]: an open source library for the reconstruction, analysis and visualization of phylogenetic trees (http://etetoolkit.org).
Technologies used: Python - *Code available:* https://github.com/etetoolkit/ete

EggNOG-mapper[3]: a program for fast functional annotation of genomes and metagenomes.
Technologies used: Python, SQL - *Code available:* https://github.com/jhcepas/eggnog-mapper

Other tasks such as the implementation of new pipelines, or providing assistance in running large scale analysis using high performance computing clusters are expected. The position offers a great opportunity to join an international network of bioinformaticians and scientific developers working on state of the art tools in the genomics field.

Requirements:

- **Resident in Madrid (required by the funding agency)**
- Bachelor degree or higher in Biotechnology, Computer Science or similar
- Good programming skills (preferably with Python experience) and Linux terminal proficiency
- Fluent English
- Motivation to learn and experiment with new technologies and big datasets
- Interest in science and research projects

Recommended additional skills:

- Knowledge in biology and genomics (i.e. Biotech degree)
- Interest in data visualization: d3, matplotlib, bokeh, etc.
- Basic experience with HPC systems, servers, and queue systems

Contract Duration: 2 years

Salary: ~19k/year gross

Deadline for applications: Jan 26th 2018

Estimated Starting Date: March-April 2018

Application process:
Send CV and motivation letter to huerta@embl.de and mark.wilkinson@upm.es

Group info: http://compgenomics.org

References:
1. Huerta-Cepas, J. *et al.* eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. *Nucleic Acids Res.* **44,** D286–93 (2016).
2. Huerta-Cepas, J., Serra, F. & Bork, P. ETE 3: Reconstruction, Analysis, and Visualization of Phylogenomic Data. *Mol. Biol. Evol.* **33,** 1635–1638 (2016).
3. Huerta-Cepas, J. *et al.* Fast genome-wide functional annotation through orthology assignment by eggNOG-mapper. *Mol. Biol. Evol.* (2017). doi:10.1093/molbev/msx148

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